Name: Tae Hoon Kim, Ph.D.

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Education:

B.A.	Reed College (Biology) 1994
M.A.	Harvard University (Molecular and Cellular Biology, with Jim Wang) 2000
Ph.D.	Harvard University (Biochemistry, with Tom Maniatis) 2002

Research Interests:
I am a functional genomicist with a broad interest in achieving systems level understanding of transcriptional regulation of the human genome.

Dissertation Title:
Structure and Function of Enhanceosome

Academic Appointments:

2002-2006	Postdoctoral Fellow (Genomics, with Bing Ren), Ludwig Institute for Cancer Research, UCSD, San Diego, CA
2006-2013	Assistant Professor, Department of Genetics, Yale University School of Medicine, New Haven, CT
2007-2014	Member, Yale Comprehensive Cancer Center, Yale University School of Medicine, New Haven, CT
2011-2014	Member, Yale Stem Cell Center, Yale University School of Medicine, New Haven, CT
2013-2014	Associate Professor, Department of Genetics, Yale University School of Medicine, New Haven, CT
2014-present	Associate Professor, Department of Biological Sciences, The University of Texas at Dallas, Richardson, TX
2014-present	Member, Center for Systems Biology, The University of Texas at Dallas, Richardson, TX
2015-2017	Founder, UTD Genome Center, The University of Texas at Dallas, Richardson, TX
2018-present	Honors Affiliate, Hobson Wildenthal Honors College, The University of Texas at Dallas, Richardson, TX
2019-present	Department Head, Department of Biological Sciences, The University of Texas at Dallas, Richardson, TX

Professional Honors & Recognition

2011	Stewart Trust Scholar Award
2008	Sidney Kimmel Scholar Award
2007	Rita Allen Scholar Award
2006	AACR Edward A. Smuckler Memorial Workshop Scholarship
2006	Korean American Scientists and Engineers Association Young Investigator Award
2005	James Kerr Award, Ludwig Institute for Cancer Research, San Diego, CA
2005	Selected Participant of International Workshop on Encoding Information in DNA Sequences organized by Government of Japan
2005	Selected Participant of Frontiers of Human Embryonic Stems Cells
2004	Ruth L. Kirschstein National Research Service Award
2002	Distinction in Teaching Award, Harvard University
1990	Korea Times Scholar
1990	Westinghouse Scholar

GRANT SUPPORT HISTORY:

Current Support

Agency: NIH/NHLBI
I.D.#: R01HL131652
Title: Defining the mechanisms of lymphatic and lymphovenous valve development
P.I.: Sathish Srinivasan
Role on project: Co-Investigator
Percent effort: 8.3%
Total costs: $1,768,000
Project period: 6/1/2016 – 5/31/2020

Past Support

Agency: NIH/NIMH
I.D.#: R21MH109945
Title: Generation of Viral Based Inducible and Cre Dependent Genome Editing Tools for Neuroscience
P.I.: Jonathan Ploski
Role on project: Co-Investigator
Percent effort: 8.3%
Total costs: $420,750
Project period: 7/1/2016 – 6/30/2018

Agency: Connecticut Department of Public Health
I.D.#: 13-SCB-Yale-06
Title: Pluripotency and Heterochromatin Topology

P.I.: Tae Hoon Kim
Percent effort: 25%
Total costs: $750,000
Project period: 11/1/2013 – 8/31/2017

Agency: <u>NIH/NIAID</u>
I.D.#: R21AI107067
Title: Nuclear, Genomic and Molecular Regulation of Type I Interferon Transcription
P.I.: Tae Hoon Kim
Percent effort: 8.3%
Total costs: $445,290
Project period: 7/1/2013 – 6/30/2017

Agency: <u>NIH/NCI</u>
I.D.#: R01CA140485
Title: Analysis of higher order chromatin structures in normal and cancer epigenomes
P.I.: Tae Hoon Kim
Percent effort: 16.7%
Total costs: $1,717,065
Project period: 7/1/2010 – 5/31/2017

Agency: <u>NIH/NIDCD</u>
I.D.#: R01DC010791
Title: Integrative systems biology approaches to auditory hair cell regeneration
P.I.: Sean Megason
Role on project: Co-Investigator
Percent effort: 5%
Total costs: $2,051,728
Project period: 2/15/2010 – 8/31/2014

Agency: <u>Yale University Department of Pharmacology</u>
I.D.#: William H. Prusoff Travel Award
P.I.: Celeste Greer
Role on project: Mentor
Percent effort: N/A
Total costs: $2,000
Project period: 8/5/2014 – 5/31/2015

Agency: <u>Yale University Department of Genetics</u>
I.D.#: Research Startup Grant
P.I.: Tae Hoon Kim
Percent effort: N/A
Total costs: $10,000
Project period: 6/26/2013 – 6/30/2014

Agency: Yale University Department of Genetics
I.D.#: Postdoctoral Fellowship for Yoon Jung Kim
P.I.: Yoon Jung Kim
Role on project: Mentor
Percent effort: N/A
Total costs: $100,000
Project period: 3/31/2012 – 6/30/2014

Agency: PhRMA Foundation
I.D.#: Predoctoral Fellowship for Celeste Greer
P.I.: Celeste Greer
Role on project: Mentor
Percent effort: N/A
Total costs: $40,000
Project period: 6/1/2011 – 5/31/2013

Agency: Alexander and Margaret Stewart Trust (Pew-Stewart Scholar Award)
I.D.#: Stewart Fellowship
Title: Targeting genomic amplicons in cancers
P.I.: Tae Hoon Kim
Percent effort: 10%
Total costs: $150,000
Project period: 7/1/2011 – 6/30/2013

Agency: Yale Cancer Center
I.D.#: Pilot Project
Title: Epigenetic modulation of breast cancer amplicons
P.I.: Tae Hoon Kim
Percent effort: 5%
Total costs: $50,000
Project period: 9/1/2009 – 8/30/2010

Agency: Sidney Kimmel Foundation for Cancer Research
I.D.#: Scholar Award SKF-8-089
Title: Analysis of chromatin barriers in cancers
P.I.: Tae Hoon Kim
Percent effort: 10%
Total costs: $200,000
Project period: 7/01/2008 – 6/30/2010

Agency: Rita Allen Foundation
I.D.#: Scholar Award 187562
Title: Analysis of insulators in cancers

P.I.: Tae Hoon Kim
Percent effort: 60%
Total costs: $250,000
Project period: 10/1/2007 – 6/30/2010

Agency: Yale University
I.D.#: Startup
Title: N/A
P.I.: Tae Hoon Kim
Percent effort: N/A
Total costs: $1,250,000
Project period: 11/20/2006 – 6/30/2012

Agency: NIH/NCI
I.D.#: F32CA108313
Title: Decoding signal transduction pathways in cancer cells
P.I.: Tae Hoon Kim
Percent effort: 100%
Total costs: $122,248
Project period: 6/1/2004 – 11/30/2006

Invited Speaking Engagements, Presentations, Symposia & Workshops:

Listed in reverse chronological order.

2019	College of Pharmacy, Chung Ang University, Seoul, Korea, "How to turn on a gene?"
2019	Biology Department Seminar, Louisiana State University, Baton Rouge, LA, "Switches and dials – finding meaning in the noncoding genome."
2016	US-Korea Conference, Dallas, TX, "Transcription Elongation in Cancers."
2016	Rita Allen Scholars Program 40th Reunion, Stanford University, Palo Alto, CA.
2016	Biology Department Seminar, Southern Methodist University, Dallas, TX, "Transcription Elongation in Cancers."
2015	Pew Scholars Program 30th Reunion, Grand Cayman Island, Cayman Island.
2015	*Distinguished Lecture*, Oklahoma Medical Research Foundation Research Forum, Oklahoma City, OK, "Transcription elongation, noncoding RNAs and chromosomal looping."
2015	Neuroscience Research Conference, The University of Texas at Dallas, Richardson, TX, "eRNAs in nervous system."

2015 Samsung Genome Institute, Samsung Medical Center, Seoul, South Korea, “Targeting Transcription Elongation Control in Cancer Therapy.”

2015 Seoul National University, Seoul, South Korea, “Targeting Transcription Elongation Control in Cancer Therapy.”

2015 University of Texas Southwestern, Hamon Center for Therapeutic Oncology & Simmons Cancer Center, Dallas, TX, “Transcription Elongation Control in Breast Cancers.”

2014 The University of Texas at Dallas, Department of Molecular and Cellular Biology, Dallas, TX, “Emerging mechanisms of transcription control in the human genome.”

2013 US-Korea Conference, East Rutherford, NJ, “Pluripotency and Heterochromatin Topology.”

2013 Rita Allen Foundation, Keynote Presentation at the Rita Allen Scholars Meeting, Norwalk, CT, “Transcription elongation control of oncogenes.”

2012 University of Pennsylvania School of Medicine, Department of Genetics, Philadelphia, PA, “Exploring new frontiers of transcriptional regulation.”

2012 University of Seoul, Korea, “Transcription insulation and elongation.”

2011 Yale University, Yale Stem Cell Center, Annual Retreat, Orange, CT, “Modulation of chromatin barrier activity during reprogramming and tumorigenesis.”

2011 Yale University School of Medicine, Yale Cancer Center, Annual Retreat, Orange, CT, “Targeting genomic amplicons in cancers.”

2010 Rita Allen Foundation, Institute for Advanced Studies, Princeton, NJ, “Higher order chromatin structures in normal and cancer epigenomes.”

2010 Yale University School of Medicine, Yale Cancer Center, Annual Retreat, Orange, CT, “Modulation of breast cancer amplicons.”

2008 Princeton University, Computer Science Department, Princeton, NJ, “Locating and analyzing genetic switches in the human genome.”

2007 7th Annual ORFeome Meeting: ORFeomes and Systems, Harvard Medical School, Boston, MA, “Genome-wide function of CTCF.”

2007 Yale University School of Medicine, Department of Genetics, New Haven, CT, “Genome-wide distribution and sequence determinant of CTCF binding.”

2007 EMBO Chromatin and Epigenetics Conference, Heidelberg, Germany, "Genome-wide distribution, sequence determinant and evolution of CTCF binding."

2007 Cold Spring Harbor Laboratory Meeting on Systems Biology, Cold Spring Harbor, NY, "Genome-wide distribution and sequence determinant of CTCF binding."

2006 Science Park Symposium, The Scripps Research Institute, San Diego, CA, "Analysis of the vertebrate insulator protein CTCF binding sites in the human genome."

2006 Montreal Microarray Symposium, Montreal, Quebec, Canada, "Locating genetic switches in the genome."

2006 Keystone Symposia on Regulation of Eukaryotic Transcription, Taos, New Mexico, "Identification and Analysis of Boundary Elements in the Human Genome."

2006 Salk Institute, San Diego, CA, "Genome-wide Analysis of Protein-DNA Interactions."

2005 Keystone Symposia on Stem Cells, Senescence and Cancer, Singapore, "Decoding the WNT Signaling Pathway."

2005 FASEB Research Conference on Transcription and Chromatin, Snowmass, CO, "A high-resolution map of active promoters in the human genome."

2005 International Workshop on Encoding Information in DNA Sequences, Okinawa, Japan, "A high-resolution map of active promoters in the human genome."

Peer-Reviewed Presentations & Symposia:

2019 Cell Symposia, Berlin, Germany. "Global transcriptional activity dynamics reveal functional enhancer RNAs."

2019 Keystone Symposia on 3D Genome, Banff, Calgary, Canada.

2017 Gordon Research Conference on Chromosome Dynamics, Italy, "Dynamic production of functional enhancer RNAs from virus-inducible enhancers"

2017 Keystone Symposia on Interferons, Banff, Calgary, Canada.

2016 Keystone Symposia on Long Noncoding RNAs and Enhancers, Santa Fe, NM.

2015 CPRIT Innovations in Cancer Prevention and Research Conference, Austin, TX.

2013 Cold Spring Harbor Laboratory Mechanisms of Eukaryotic Transcription Meeting, Cold Spring Harbor, NY, "HDAC inhibitors induce transcriptional repression of high copy number genes in breast cancer through elongation blockade."

2012 ASCO Annual Meeting, Chicago, IL, "ERβ mRNA expression in ERα-negative and triple negative breast cancers."

2009: Cold Spring Harbor Laboratory Mechanisms of Eukaryotic Transcription Meeting, Cold Spring Harbor, NY, "Higher order chromatin structure and expression at the HOXA locus."

2007: Cold Spring Harbor Laboratory Mechanisms of Eukaryotic Transcription Meeting, Cold Spring Harbor, NY, "Genome-wide function of CTCF."

PROFESSIONAL SERVICE

Listed in reverse chronological order.

Peer Review Groups/Grant Study Sections:

2019	Temporary Member, Career Development Subcommittee (NCI-J), NIH/NCI
2017	Member, Program Grant Review Committee, NIH/NCI
2016-present	Member, Genome Research Review Committee (GNOM-G), NIH/NHGRI
2016	Temporary member, Genome Research Review Committee (GNOM-G), NIH/NHGRI
2015	Member, 4D Nucleome Study Section, NIH
2014	Temporary member, GCAT Study Section, NIH
2014	Reviewer, King's Health Partners, UK
2013-2014	Reviewer, Medical Research Council, UK
2012	Temporary member, GCAT Study Section, NIH
2011	Reviewer, Breast Cancer Campaign
2010	Member, Special Emphasis Panel, NIH/NCI
2010-2012	Member, Italian Ministry of Health
2009-2013	Member, Committee on DNA Mechanisms of Cancer, American Cancer Society
2009-2010	Member, Gene Expression Advisory Panel, Gene and Genome Systems Cluster, National Science Foundation
2009	Member, Association of International Cancer Research

Journal Service:

Editor

2014	Editor for Journal of Molecular Biology

Reviewer

2007-present Reviewer for *Nature, Cell, Nature Genetics, Nature Biotechnology, Nature Communications, Genes & Development, Current Biology, Genome Research, PLoS Biology, PLoS Genetics, Proceedings of National Academy of Sciences USA, EMBO, Cell Reports, Genome*

Biology, Experimental Cell Research, BMC Neuroscience, Molecular Cancer Research, Nucleic Acids Research, Journal of Molecular Biology, JOVE

Professional Service for Professional Organizations:

Global Alliance for Genomics and Health

2017-Present	Member

American Association for Cancer Research

2006-present	Member

Rita Allen Foundation

2011-2015	Member, Planning Committee for Scholars Program, Rita Allen Foundation

Korean-American Scientists and Engineers Association (KSEA)

2016	Chair, Systems Biology and Bioinformatics Session, US-Korea Conference, Dallas, Texas

The University of Texas at Dallas:

University Committees

2019-present	Vice Chair, Committee on Distance Learning
2019	Reviewer, *ad hoc* review committee for emeritus title conferment (Dennis Miller)
2019	Reviewer, *ad hoc* review committee for emeritus title conferment (Gail Breen)
2019	Member, Provost's Task Force on Online Education
2018	Reviewer, Office of Research Core Facilities Voucher Seed Program
2018	Chair, *ad hoc* committee for Promotion and Tenure Review (Duane Winkler)
2018	Member, NSM Committee on Faculty Teaching Workload Policy
2016-2018	Member, Institutional Biosafety and Chemical Safety Committee
2017	Chair, *ad hoc* committee for Mid-Probationary Review (Zachary Campbell)
2016	Chair, *ad hoc* committee for Promotion and Tenure Review (Zhenyu Xuan)
2015-present	Member, SKKU (Sunkyunkwan University) Scholarship Committee
2015	Member, *ad hoc* committee for Mid-Probationary Review (Heng Du)
2014-2015	Member, School of Natural Sciences and Mathematics Bylaws Committee
2014-2017	Founder & Organizer, Grants Club - a peer-support group that brings together faculty across UTD to discuss laboratory management and grants. Members received 4 R01 and 2 R21 grants from NIH during the years that I have organized the meetings.

Departmental Committees

2018	Member, Biological Sciences Faculty Search Committee
2016	Chair, Biological Sciences Faculty Search Committee
2014-2015	Member, Biological Sciences Faculty Search Committee

Yale University:

2011-2014	Member, Genetics Faculty Search Committee
2011	Reviewer, Yale Cancer Center Pilot Project application
2009-2014	Member, Systems Biology Institute Advisory Committee, Yale University
2010	Participant, Stewart Trust Site Visit, Yale Cancer Center
2010	Member, Genetics Steering Committee
2007-2008	Organizer, Genetics Department Annual Retreat
2006-2009, 2012	Member, MCGD Graduate Admissions Committee, Yale University

Public Service:

2019-present	
2018-present	Volunteer, City of Plano, Texas
2016-2018	Member, School-Based Improvement Committee, Huffman Elementary School
2015	Judge, TX BEST Robotics Regional Championship

Bibliography:

Listed in chronological order. >10,250 citations. *H*-index 22. Underlined are students or fellows under my direct supervision.

Peer-Reviewed Original Research

1. **Tae Hoon Kim**. Expression of Salt Tolerance Genes in *Vibrio costicola. BASE: A Journal of Science and Technology* 8:6-10 (1990).
2. Tae Kook Kim, **Tae Hoon Kim**, and Tom Maniatis. Efficient recruitment of TFIIB and CBP-RNA polymerase II holoenzyme by an Interferon-β enhanceosome in vitro. *Proceedings of National Academy of Sciences, USA* 95:12191-96 (1998).
3. Tom Maniatis, James Falvo, **Tae Hoon Kim**, Tae Kook Kim, Charles H. Lin, Bhavin S. Parekh, and Marc G. Wathelet. Structure and function of the interferon-β enhanceosome. *Cold Spring Harbor Symposium on Quantitative Biology* 63:609-620 (1998).
4. Bing Ren, Kerlen J. Chee, **Tae Hoon Kim**, and Tom Maniatis. PRDI-BF1/Blimp-1 repression is mediated by corepressors of the groucho family of proteins. *Genes and Development* 13:125-137 (1999).
5. **Tae Hoon Kim**, Hui Xong, Zhuohua Zhang, and Bing Ren. β-catenin activates the growth factor endothelin-1 in colon cancer cells. *Oncogene* 24:597-604 (2005).

6. **Tae Hoon Kim**, Leah O. Barrera, Chunxu Qu, Sara Van Calcar, Nathan Trinklein, Sarah Hartman, Rosa Luna, Christopher K. Glass, Michael G. Rosenfeld, Richard Myers, and Bing Ren. Direct isolation and identification of promoters in the human genome. *Genome Research* 15:830-839 (2005).
7. **Tae Hoon Kim**, Leah O. Barrera, Ming Zheng, Chunxu Qu, Michael A. Singer, Todd A. Richmond, Yingnian Wu, Roland Green, and Bing Ren. A high-resolution map of active promoters in the human genome. *Nature* 436:876-880 (2005).
8. Ping Sun, Hui Xiong, **Tae Hoon Kim**, Bing Ren, and Zhuohua Zhang. Positive Inter-Regulation between Beta-Catenin/T Cell Factor-4 Signaling and Endothelin-1 Signaling Potentiates Proliferation and Survival of Prostate Cancer Cells. *Molecular Pharmacology* 69:520-31 (2006).
9. **Tae Hoon Kim***, Ziedulla Abdullayev, Keith A. Ching, Andrew Smith, Dmitri Loukinov, Roland D. Green, Michael Q. Zhang, Victor Lobanenkov and Bing Ren*. Analysis of the vertebrate insulator protein CTCF binding sites in the human genome. *Cell* 128:1231-1245 (2007). *corresponding authors
10. The ENCODE Project Consortium. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature* 447:799-816 (2007).
11. Kerrigan B. Gilbert, **Tae Hoon Kim**, Rashmi Gupta, E. P. Greenberg, and Martin Schuster. Global position analysis of the *Pseudomonas aeruginosa* quorum-sensing transcription factor LasR. *Molecular Microbiology* 73:1072-1085 (2009).
12. Yoon Jung Kim, Katharine R. Cecchini and **Tae Hoon Kim**. Conserved, developmentally regulated mechanism couples chromosomal looping and heterochromatin barrier activity at the homeobox gene A locus. *Proceedings of National Academy of Sciences, USA* 108:7391-7396 (2011).
13. Bora E. Baysal, Sharen E. McKay, Yoon Jung Kim, Zimei Zhang, Linda Alila, Joan E. Willett-Brozick, Karel Pacak, **Tae Hoon Kim** and Gerald S. Shadel. Genomic imprinting at a boundary element flanking the SDHD locus. *Human Molecular Genetics* 20:4452-4461 (2011).
14. Yoon Jung Kim*, Celeste Greer*, Katharine R. Cecchini, Lyndsay N. Harris, David P. Tuck and **Tae Hoon Kim**. HDAC inhibitors induce transcriptional repression of high copy number genes in breast cancer through elongation blockade. *Oncogene* 32: 2828-2835 (2013). *equal contribution
15. Lark Kyun Kim, Enric Esplugues, Cornelia E. Zorca, Fabio Parisi, Yuval Kluger, **Tae Hoon Kim**, Niels J. Galjart, and Richard A. Flavell. Oct-1 regulates IL-17 expression by directing interchromosomal associations in conjunction with CTCF in T cells. *Molecular Cell* 54:56-66 (2014).
16. A. Raja Banerjee*, Yoon Jung Kim* and **Tae Hoon Kim**. A novel virus-inducible enhancer functionally associated with the interferon-β gene with tightly linked promoter and enhancer activities. *Nucleic Acid Research* 42:12537-54 (2014). *equal contribution
17. Ifeoma Jane Nwigwe, Yoon Jung Kim, David A. Wacker and **Tae Hoon Kim**. Boundary associated long noncoding RNA mediates long-range chromosomal interactions. *PLoS ONE* 10(8):e0136104 (2015).

18. Celeste B. Greer, Yoshiaki Tanaka, Yoon Jung Kim, Peng Xie, Michael Q. Zhang, In-Hyun Park and **Tae Hoon Kim**. Histone deacetylases positively regulate transcription through the elongation machinery. *Cell Reports* 13:1444-1455 (2015).
19. Qianqian Ye, Yoon Jung Kim, Hongyu Zhao and **Tae Hoon Kim**. Three distinct velocities of elongating RNA polymerase define exons and introns. *bioRxiv* doi:10.1101/044123 (2016).
20. Justin L. Tan, Rachel D. Fogley, Ryan A. Flynn, Julien Ablain, Song Yang, Violaine Saint-André, Zi Peng Fan, Brian T. Do, Alvaro C. Laga, Koh Fujinaga, Cristina Santoriello, Celeste B. Greer, Yoon Jung Kim, John G. Clohessy, Anne Bothmer, Nicole Pandell, Serine Avagyan, John E. Brogie, Ellen van Rooijen, Elliot J. Hagedorn, Ng Shyh-Chang, Richard M. White, David H. Price, Pier Paolo Pandolfi, B. Matija Peterlin, Yi Zhou, **Tae Hoon Kim**, John M. Asara, Howard Y. Chang, Richard A. Young and Leonard I. Zon. Stress from Nucleotide Depletion Activates the Transcriptional Regulator HEXIM1 to Suppress Melanoma. *Molecular Cell* 62:34-46 (2016).
21. Boksik Cha, Xin Geng, Md. Riaj Mahamud, Jianxin Fu, Anish Mukherjee, Yeunhee Kim, Eek-hoon Jho, **Tae Hoon Kim**, Mark L. Kahn, Lijun Xia, J. Brandon Dixon, Hong Chen, and R. Sathish Srinivasan. Mechanotransduction activates canonical Wnt/β-catenin signaling to promote lymphatic vascular patterning and the development of lymphatic and lymphovenous valves. *Genes & Development* 30:1454-1469 (2016).
22. Brian S. Johnson, Yingtao Zhao, Maria D. Fasolino, Janine M. Lamonica, Yoon Jung Kim, Katie H. Wood, Daniel Bu, Yue Cui, Darren Goffin, **Tae Hoon Kim** and Zhaolan Zhou. Biotin tagging of MeCP2 reveals contextual insights into the Rett syndrome transcriptome. *Nature Medicine* 23:1203-1214 (2017). PMC5630512
23. Pradipta Ray, Andrew Torck, Lilyana Quigley, Andi Wangzhou, Matthew Neiman, Chandranshu Rao, Tiffany Lam, Ji-Young Kim, **Tae Hoon Kim**, Michael Q. Zhang, Gregory Dussor and Theodore J. Price. Comparative transcriptome profiling of the human and mouse dorsal root ganglia: An RNA-seq-based resource for pain and sensory neuroscience research. *Pain* 159:1325-1345 (2018).
24. **Tae Hoon Kim*** and Job Dekker*. Chromatin Immunoprecipitation (ChIP) analysis of protein-DNA interactions. *Cold Spring Harbor Protocols* doi:10.1101/pdb.top082586 (2018). *corresponding authors
25. **Tae Hoon Kim*** and Job Dekker*. ChIP-seq. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot082644 (2018). *corresponding authors
26. **Tae Hoon Kim*** and Job Dekker*. ChIP-chip. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot082636 (2018). *corresponding authors
27. **Tae Hoon Kim*** and Job Dekker*. ChIP-Quantitative Polymerase Chain Reaction (ChIP-qPCR). *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot082628 (2018). *corresponding authors
28. **Tae Hoon Kim*** and Job Dekker*. ChIP. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot082610 (2018). *corresponding authors
29. **Tae Hoon Kim*** and Job Dekker*. Preparation of Cross-Linked Chromatin for ChIP. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot082602 (2018). *corresponding authors

30. **Tae Hoon Kim*** and Job Dekker*. Formaldehyde Cross-Linking. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot082594 (2018). *corresponding authors
31. **Tae Hoon Kim*** and Job Dekker*. Generation of 3C Libraries from Cross-linked Cells. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot097840 (2018). *corresponding authors
32. **Tae Hoon Kim*** and Job Dekker*. Generation of Control Ligation Product Libraries for 3C Analyses. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot097865 (2018). *corresponding authors
33. **Tae Hoon Kim*** and Job Dekker*. Generation of ChIP-loop libraries. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot097857 (2018). *corresponding authors
34. **Tae Hoon Kim*** and Job Dekker*. 3C-Based Chromatin Interaction Analyses. *Cold Spring Harbor Protocols* doi:10.1101/pdb.top097832 (2018). *corresponding authors
35. **Tae Hoon Kim*** and Job Dekker*. Polymerase Chain Reaction (PCR) Detection of 3C Ligation Products Present in 3C, ChIP-Loop, and Control Libraries: Library Titration and Interaction Frequency Analysis. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot097873 (2018). *corresponding authors
36. **Tae Hoon Kim*** and Job Dekker*. 4C Analysis of 3C, ChIP-loop, and control libraries. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot097881 (2018). *corresponding authors
37. **Tae Hoon Kim*** and Job Dekker*. 5C Analysis of 3C, ChIP-loop, and control libraries. *Cold Spring Harbor Protocols* doi:10.1101/pdb.prot097899 (2018). *corresponding authors
38. Ying-Tao Zhao, Deborah Y. Kwon, Brian S. Johnson, Maria Fasolino, Janine M. Lamonica, Yoon Jung Kim, Boxuan Simen Zhao, Chuan He, Golnaz Vahedi, **Tae Hoon Kim** and Zhaolan Zhou. Long genes linked to autism spectrum disorders harbor broad enhancer-like chromatin domains. *Genome Research* 28:933-942 (2018).
39. Boksik Cha, Xin Geng, Md. Riaj Mahamud, Jenny Y. Zhang, Lijuan Chen, Wantae Kim, Eek-hoon Jho, Yeunhee Kim, Dongwon Choi, J. Brandon Dixon, Hong Chen, Young-Kwon Hong, Lorin Olson, **Tae Hoon Kim**, Bradley J. Merrill, Michael J. Davis, R. Sathish Srinivasan. Complementary Wnt Sources Regulate Lymphatic Vascular Development via PROX1-Dependent Wnt/β-Catenin Signaling. *Cell Reports* 25:571-584 (2018).
40. Yoon Jung Kim*, Peng Xie*, Lian Cao, Michael Q. Zhang and **Tae Hoon Kim**. Global transcriptional activity dynamics reveal functional enhancer RNAs. *Genome Research* 28:1799-1811 (2018). *equal contribution
41. Robert Y. North, Yan Li, Pradipta Ray, Laurence D Rhines, Claudio Esteves Tatsui, Ganesh Rao, Caj A. Johansson, Hongmei Zhang, Yeun Hee Kim, Bo Zhang, Gregory Dussor, **Tae Hoon Kim**, Theodore J. Price and Patrick M. Dougherty. Electrophysiological and transcriptomic correlates of neuropathic pain in human dorsal root ganglion neurons. *Brain* 142:1215-1226 (2019).
42. Meng-Hsiung Hsieh, Joshua H. Choe, Jashkaran Gadhvi, Yoon Jung Kim, Marcus A. Arguez, Madison Palmer, Haleigh Gerold, Chance Nowak, Hung Do, Simbarashe Mazambani, Jordan K. Knighton, Matthew Cha, Justin Goodwin, Min Kyu Kang, Ji Yun Jeong, Shin Yup Lee, Brandon Faubert, Zhenyu Xuan, E. Dale Abel, Claudio Scafoglio, David B. Shackelford, John D. Minna, Pankaj K. Singh, Vladimir Shulaev, Leonidas Bleris, Kenneth Hoyt, James Kim, Masahiro Inoue, Ralph J. DeBerardinis, **Tae Hoon Kim** and Jung-whan Kim. p63 and SOX2

Dictate Glucose Reliance and Metabolic Vulnerabilities in Squamous Cell Carcinomas. *Cell Reports* 28:1860-1878 (2019).

43. Md Riaj Mahamud, Xin Geng, Yen-Chun Ho, Boksik Cha, Yeunhee Kim, Jing Ma, Lijuan Chen, Greggory Myers, Sally Camper, Debbie J Mustacich, Marlys Witte, Dongwon Choi, Young-Kwon Hong, Hong Chen, Gaurav Varshney, James Engel, Shusheng Wang, **Tae Hoon Kim**, Kim-Chew Lim and Sathish Srinivasan. GATA2 controls lymphatic endothelial cell junctional integrity and lymphovenous valve morphogenesis through miR126. *Development* (2019).

Chapters, Books, and Reviews

44. **Tae Hoon Kim**. *Programmed Cell Death in Arabidopsis thaliana*. Reed College. Portland (1994).
45. **Tae Hoon Kim**. *Structure and Function of Enhanceosome*. Harvard University. Cambridge (2002).
46. **Tae Hoon Kim** and Bing Ren. All-around view of eukaryotic transcription. *Genome Biology* 7:323 (2006).
47. **Tae Hoon Kim*** and Bing Ren*. Genome-wide Analysis of Protein-DNA Interactions. *Annual Review of Genomics and Human Genetics* 7:81-102 (2006). *corresponding authors
48. **Tae Hoon Kim***, Leah O. Barrera and Bing Ren*. ChIP-chip for genome-wide analysis of protein binding in mammalian cells. *Current Protocols in Molecular Biology* 79 Unit 21.13 (2007). *corresponding authors
49. David A. Wacker and **Tae Hoon Kim**. From Sextant to GPS: Twenty-five Years of Mapping the Genome with ChIP. *Journal of Cellular Biochemistry* 107:6-10 (2009).
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